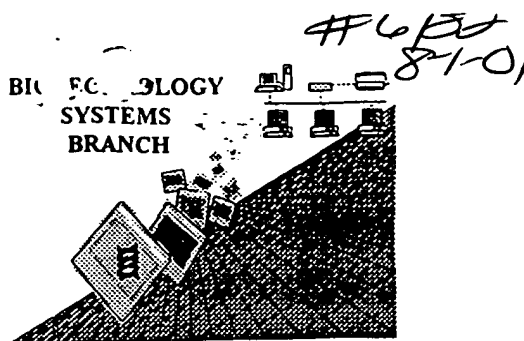


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/716,356

Source: OIPE

Date Processed by STIC: 5-31-01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/716, 356

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                               (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                               <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9 ✓ Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                               Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ✓ Use of <220>     Sequence(s) 9-13 ~~missing the <220> "Feature" and associated numeric identifiers and responses.~~  
                               ~~Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."~~  
                               Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,356

DATE: 05/31/2001

TIME: 16:00:38

Input Set : A:\Ushio2.app

Output Set: C:\CRF3\05312001\I716356.raw

3 <110> APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKY  
 4 USHIO, Shimpei  
 5 TORIGOE, Kakuji  
 6 TANIMOTO, Tadao  
 7 OKAMURA, Haruki  
 8 KURIMOTO, Masashi  
 9 FUKUDA, Shigeharu  
 10 KUNIKATA, Toshio  
 11 TANIGUCHI, Mutsuko  
 12 KOHNO, Keizo  
 14 <120> TITLE OF INVENTION: INTERFERON-Y INDUCING POLYPEPTIDE, PHARMACEUTICAL  
 15 COMPOSITION THEREOF, MONOCLONAL ANTIBODY THERETO, AND  
 16 METHODS OF USE  
 18 <130> FILE REFERENCE: USHIO=2  
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/716,356  
 21 <141> CURRENT FILING DATE: 2000-11-21  
 23 <150> PRIOR APPLICATION NUMBER: 08/832,198  
 24 <151> PRIOR FILING DATE: 1997-04-08  
 26 <150> PRIOR APPLICATION NUMBER: 08/721,018  
 27 <151> PRIOR FILING DATE: 1996-09-26  
 29 <150> PRIOR APPLICATION NUMBER: 08/558,191  
 30 <151> PRIOR FILING DATE: 1995-11-15  
 32 <150> PRIOR APPLICATION NUMBER: 08/832,180  
 33 <151> PRIOR FILING DATE: 1997-04-08  
 35 <150> PRIOR APPLICATION NUMBER: 08/558,818  
 36 <151> PRIOR FILING DATE: 1995-11-15  
 38 <150> PRIOR APPLICATION NUMBER: 08/832,177  
 39 <151> PRIOR FILING DATE: 1997-04-08  
 41 <150> PRIOR APPLICATION NUMBER: 08/599,879  
 42 <151> PRIOR FILING DATE: 1996-02-14  
 44 <150> PRIOR APPLICATION NUMBER: 08/974,469  
 45 <151> PRIOR FILING DATE: 1996-02-14  
 47 <160> NUMBER OF SEQ ID NOS: 22  
 49 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply  
 Corrected Diskette Needed  
 p 2, 3, 4

## ERRORED SEQUENCES

131 <210> SEQ ID NO: 4  
 132 <211> LENGTH: 157  
 133 <212> TYPE: PRT  
 134 <213> ORGANISM: MOUSE  
 136 <400> SEQUENCE: 4  
 137 Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn  
 138 1 5 10 15  
 140 Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met  
 141 20 25 30

*see p. 2.*

## RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/716,356

TIME: 16:00:38

Input Set : A:\Ushio2.app

Output Set: C:\CRF3\05312001\I716356.raw

```

143 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile
144      35      40      45
146 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser
147      50      55      60
E--> 149 Val Lys Asp Ser Lys (Xaa) Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile
150      65      70      75      80
152 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser
153      85      90      95
155 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu
156      100      105      110
158 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu
159      115      120      125
161 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
162      130      135      140
164 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
165 145      150      155
222 <210> SEQ ID NO: 6
223 <211> LENGTH: 157
224 <212> TYPE: PRT
225 <213> ORGANISM: HUMAN
227 <400> SEQUENCE: 6
228 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
229 1      5      10      15
231 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
232      20      25      30
234 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
235      35      40      45
237 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
238      50      55      60
E--> 240 Ser Val Lys Cys Glu Lys Ile Ser (Xaa) Leu Ser Cys Glu Asn Lys Ile
241      65      70      75      80
243 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
244      85      90      95
246 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
247      100      105      110
249 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
250      115      120      125
252 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
253      130      135      140
255 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
256 145      150      155
342 <210> SEQ ID NO: 8
343 <211> LENGTH: 193
344 <212> TYPE: PRT
345 <213> ORGANISM: HUMAN
347 <400> SEQUENCE: 8
348 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
349 1      5      10      15
351 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn

```

*missing mandatory**<220> to <223>**features to**explain the "Xaa"**in the sequence.**See #9 on the**Error Summary**sheet.**"Xaa" in**sequence #6**g/so.*

## RAW SEQUENCE LISTING

DATE: 05/31/2001

PATENT APPLICATION: US/09/716,356

TIME: 16:00:38

Input Set : A:\Ushio2.app

Output Set: C:\CRF3\05312001\I716356.raw

```

352          20          25          30
354 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
355          35          40          45
357 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
358          50          55          60
360 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
361 65          70          75          80
363 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
364          85          90          95
E--> 366 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
367          100         105         110
369 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
370          115         120         125
372 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
373          130         135         140
375 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
376 145          150         155         160
378 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
379          165         170         175
381 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
382          180         185         190
384 Asp

```

"Xaa" in  
sequence # 8.  
also.

## Seg # 9

<210> 9  
☐  
 <211> 20  
☐  
 <212> DNA  
☐  
 <213> Unknown  
☐

<220>  
☐

<223> Description of Unknown Organism: UNKNOWN

<400> 9  
☐

atrtcrtcdatrttctggg

☐

<210> 10 Seg # 10  
☐

<211> 20  
☐

<212> DNA  
☐

<213> Unknown  
☐

☐

<220>  
☐

<223> Description of Unknown Organism: UNKNOWN

☐

☐

<400> 10  
☐

ttygargaya tgaagayt

— What is the source of the genetic material in the unknown sequence? See # 11 on the Error Summary Sheet. (See also sequences 11, 12, 13 for same error.)

— Sequences 9, 10 are missing mandatory <220> to <223> features to explain the "n's" in the sequence. See #9 on the Error Summary Sheet.

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

F.Y.I.  
 →

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/716,356

DATE: 05/31/2001

TIME: 16:00:39

Input Set : A:\Ushio2.app

Output Set: C:\CRF3\05312001\I716356.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:149 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4  
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:240 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6  
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:366 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8  
L:397 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9  
L:397 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:409 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:409 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10